

The Need for the Review and Understanding of SELDI/MALDI Data Prior to Analysis (Analyzer Beware)

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WINDOW INTO DISEASES

Plasma Serum Urine

Effusions

Mucous Saliva Fecal Matter

Tissue (PAP; Urinary Sediment)

Bile CSF Sweat

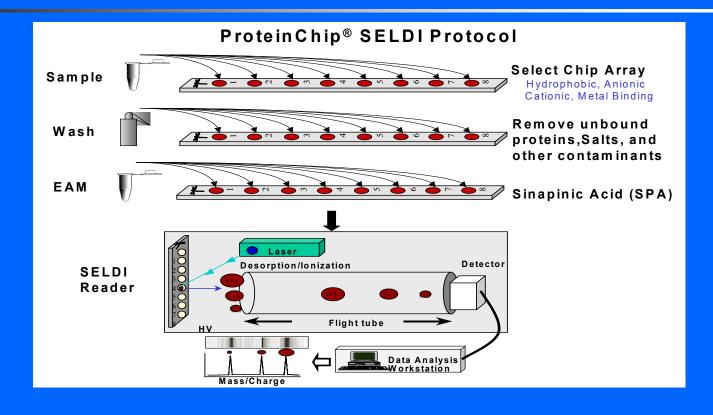
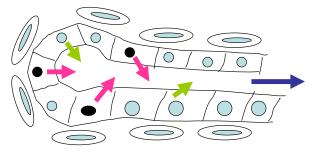
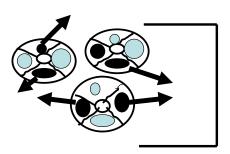


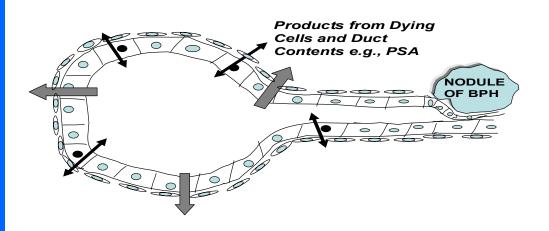
Illustration of SELDI Time-Of-Flight (TOF) Mass Spectrometry. (Modified with permission from Ciphergen Biosystems, Inc.)

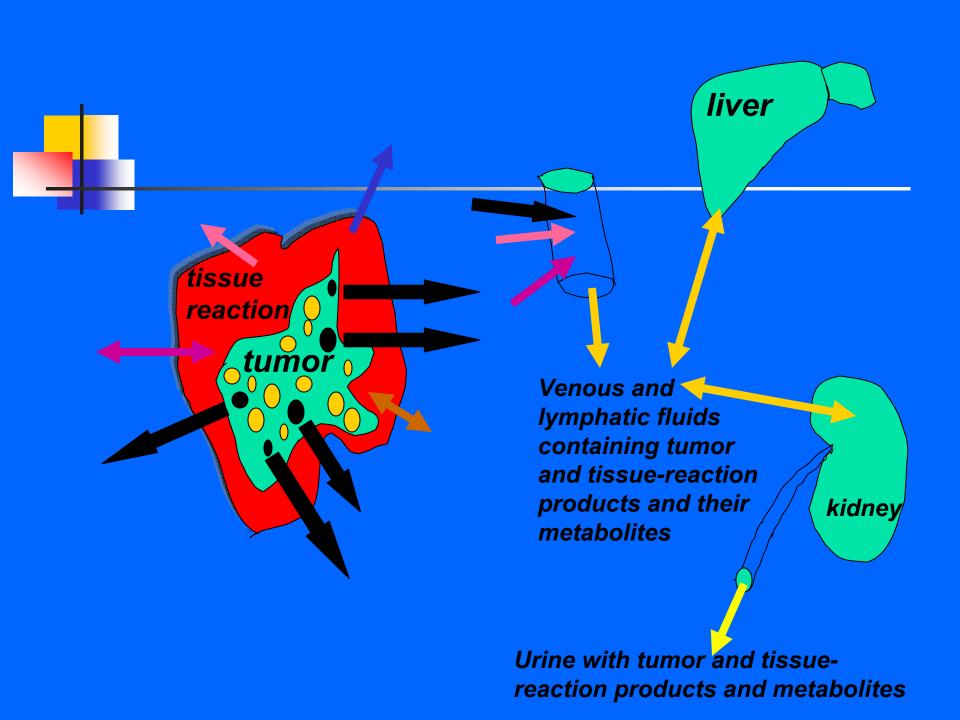


Contents of Duct Including Products of Dying Cells and Living Cells e.g., PSA

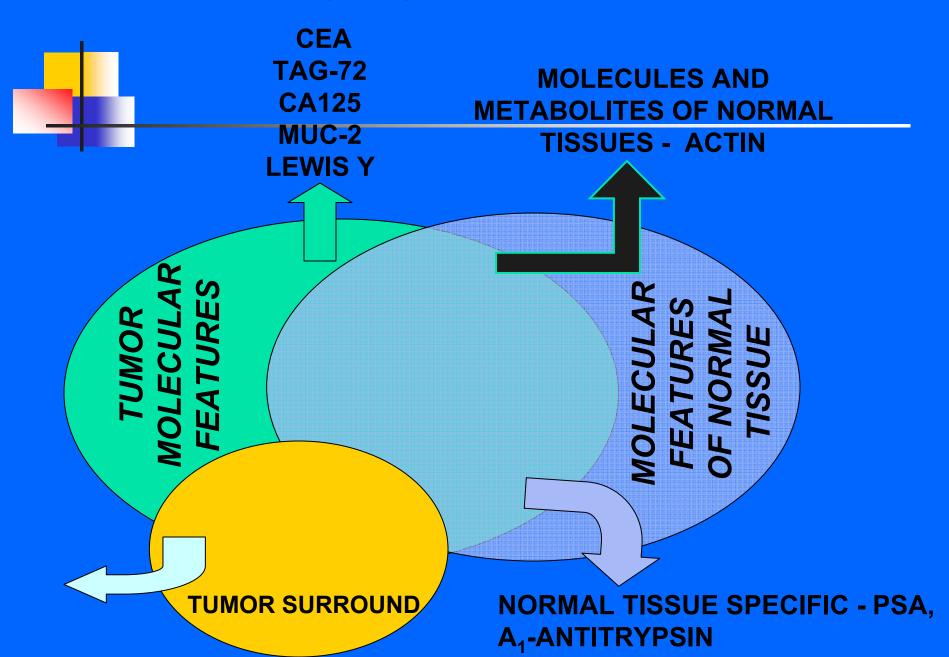


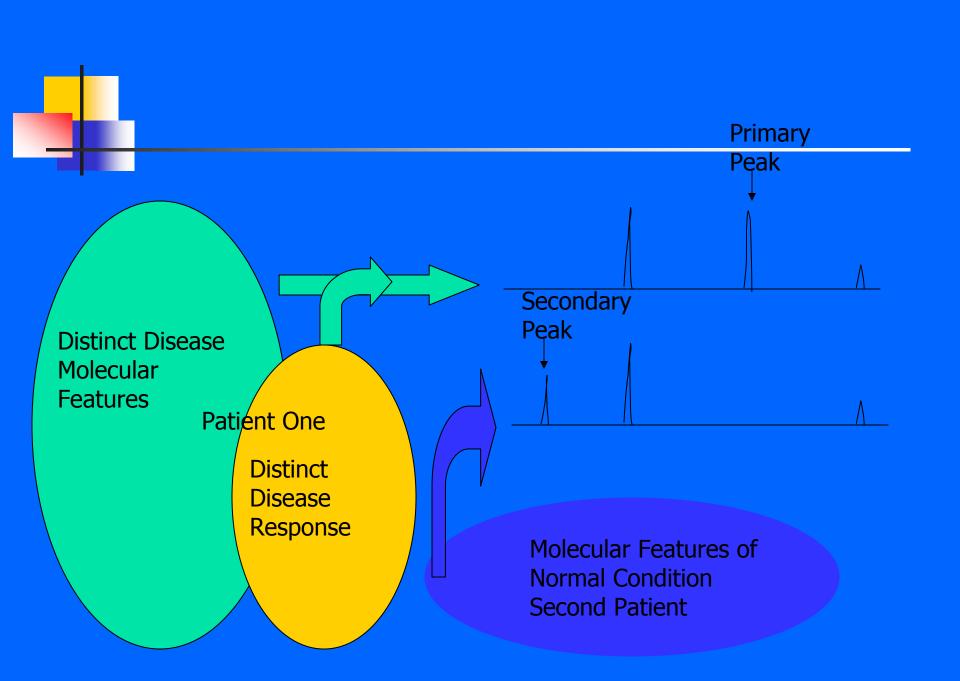
Products of Dying Cancer Cells Collect in Interstitial Space and are Absorbed into Vascular and Lymphatic Vessels





ONCOFETAL TUMOR ANTIGENS AND METABOLITES







JUNK ⇒

Statistician

Bioinformatician

⇒ JUNK

PROBLEMATIC ISSUES IN ANALYSIS

Experimental Design

Patient

Sample

Protein Chip

Spectra

Analytical Approach



Experimental Design

Selecting Cases and Controls

Collecting and Processing Samples

Performing Assays Without Bias

Selecting Optimal Approach to Analysis

Avoiding Over-Analysis



PATIENT

Groups Comparable

Sites

Racial/Ethnic Balance

Homeostatic Balance

No Bias



PATIENT

Usually Comparing Disease vs. Control or

Disease A vs. Condition B vs. Normal



PATIENT

Control Definition

Is Disease Absent?

Is There Bias In The Controls?



SAMPLE

Type

Collection

Processing

Storage

Transfer



SAMPLE

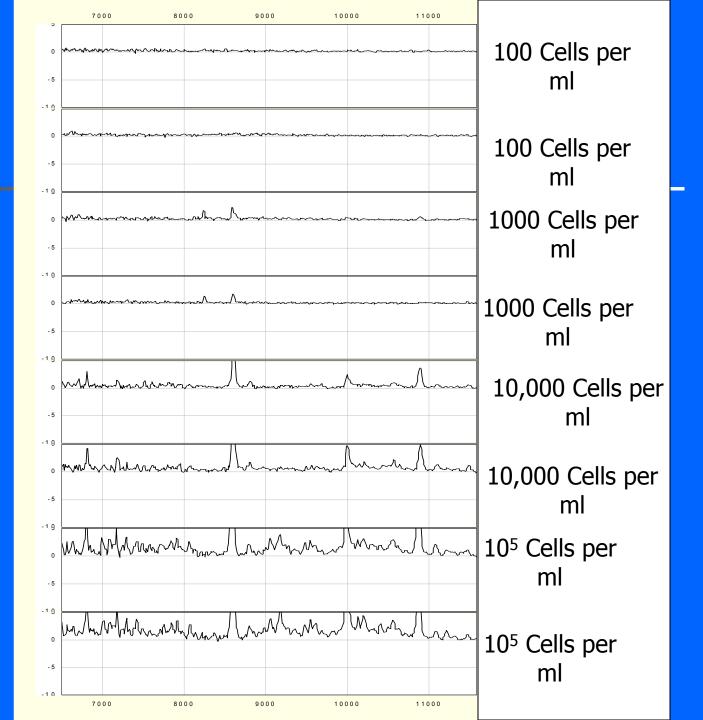
Type

Serum versus Plasma

Sensitivity- Can Products of Tumors Be Detected



LNCAP CELL LYSATES USING WCX2 ARRAYS



SAMPLE

Collection

How?

Stress

Container-e.g.., multiple anticoagulants; thus all Plasmas are not the Same

SAMPLE

Processing

Time from Collection to Freezing (Too Restrictive?)

For Consistent Results, Robotic Processing Is Required

SAMPLE

Processing

Removal of Proteins Present in Large Concentrations (e.g., Albumin) May Also Remove Peptides Being Carried by Removed Proteins

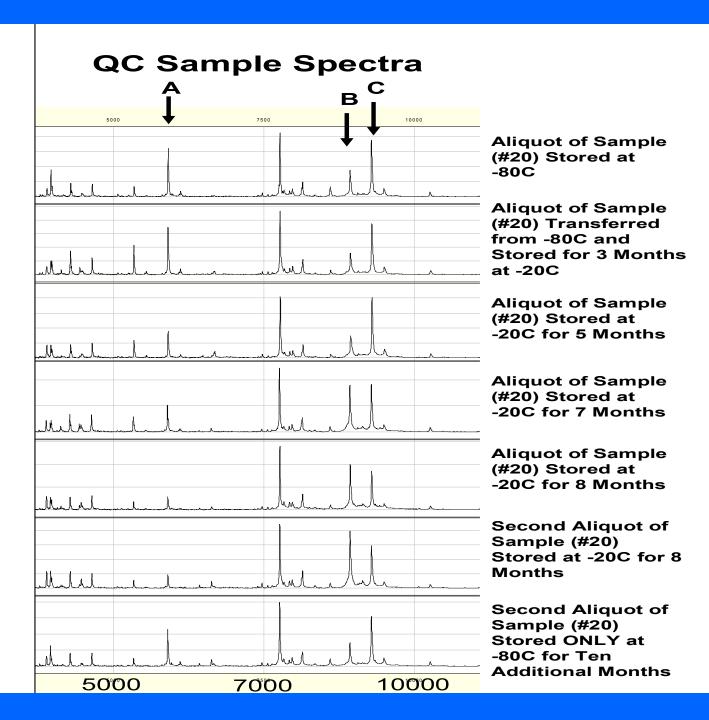


SAMPLE

Storage

Length

Temperature

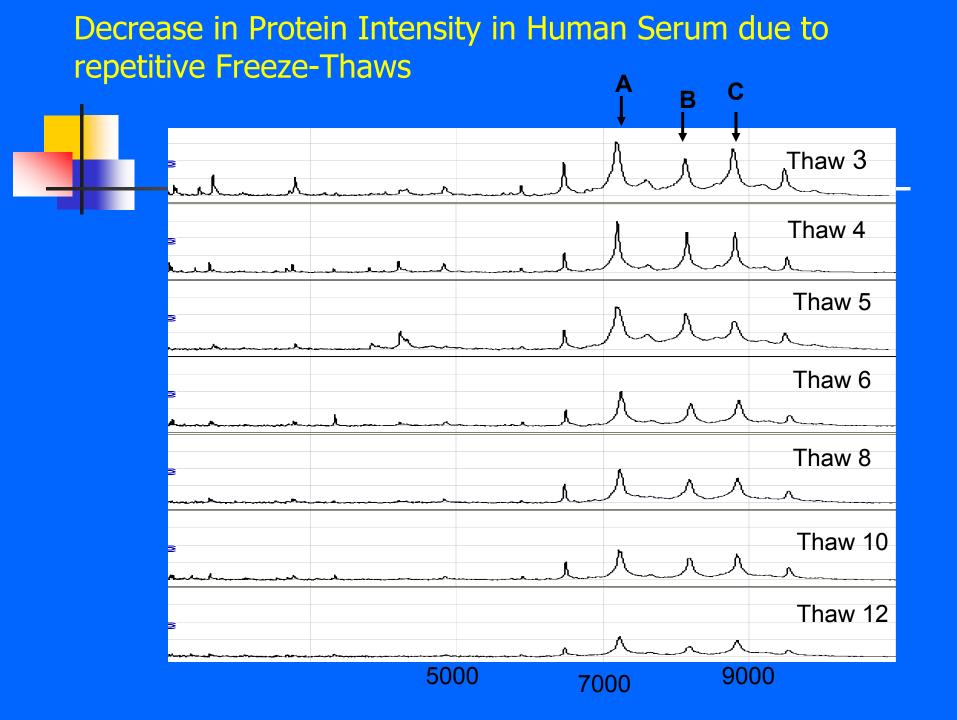




Transfer

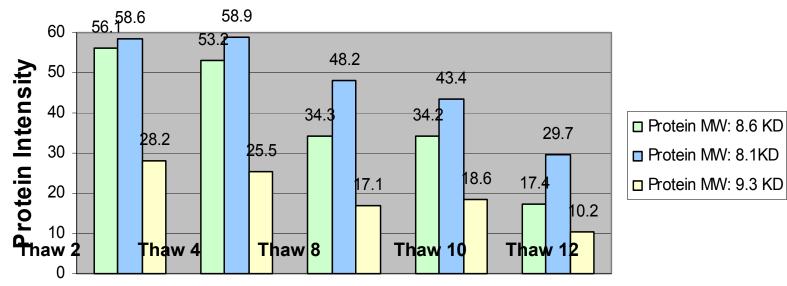
Freeze-Thaw Cycles

Quantity (Triplicates and Repeat-300 mcl)





Decrease in Protein Intensity in Human Serum (#6) due to repetitive Freeze-Thaws



Number of Freeze-Thaws

Figure 1: The graph above shows the decrease in protein intensities in three different proteins in one human serum sample. The legend indicates the molecular weight of each protein. The specific intensity values are displayed above each of the bars.

Chip Type



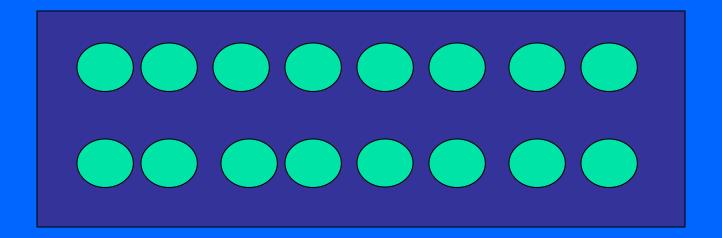
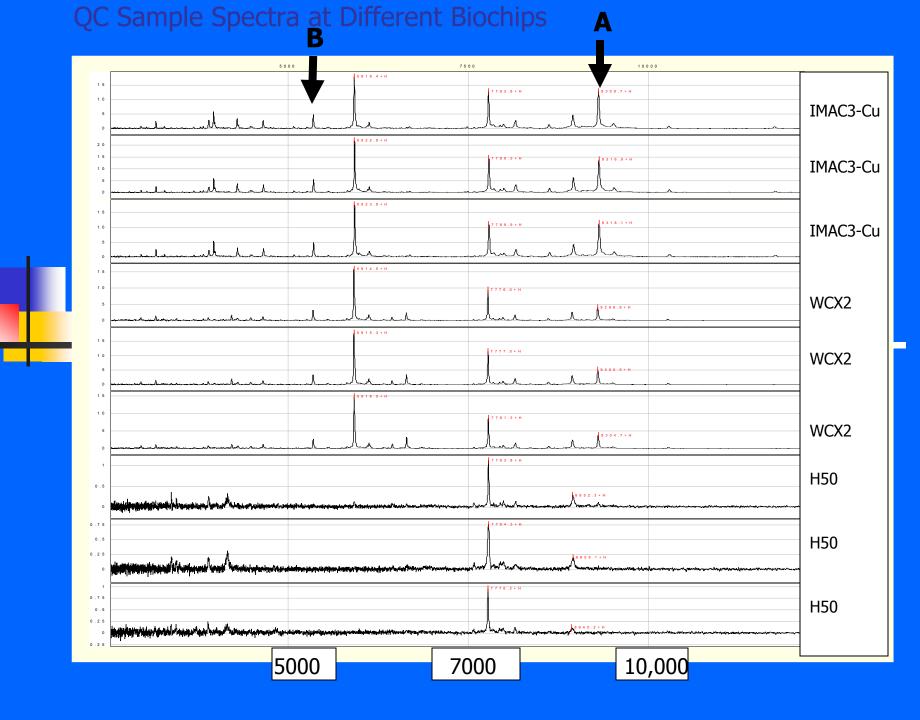


TABLE 1:

Old Designation	Current Chip	Biochemical Action of Surface Chemistry
IMAC3	IMAC30 (with hydrophobic	Bivalent metals can be attached to the chip. Proteins that bind to these divalent metals (e.g., Cu ⁺²) are bound
	barrier)	by the chip.
WCX2	Same	This is a weak cation exchange chip. It contains
	(CM10 mimics	negatively charged (anionic) carboxylate groups that
	WCX2 but does	will bind proteins with positively charged areas
	not replace it)	containing high numbers of lysine, arginine, and/or
		histidine amino acids.
H4	Same (C16	The chip contains multiple chains of 16 methylene
	contains 16 CH ₃)	groups. This binds molecules that are hydrophobic.
SAX2	Q10 (with	Strong anion exchanger which is composed of
	hydrophobic	quaternary ammonium groups that are charged
	barrier)	positively. This chip will bind proteins/peptides with
		regions rich in acidic groups, especially regions of
		peptides high in aspartic and/or glutamic amino acids.
NP1 and NP2	NP20	General protein binding surface with binding of
		hydrophilic proteins.
PS1 and PS2	PS10 / PS20	Chip designed to bind capture molecules of choices e.g.,
		antibodies, receptors, and nuclei acid binding proteins
		PS-1 (carbonyl diimidazole groups), PS-2 (epoxy
		groups). Also the PS-2 has a hydrophobic coating.
SENDID		Incorporates EAM into chip.



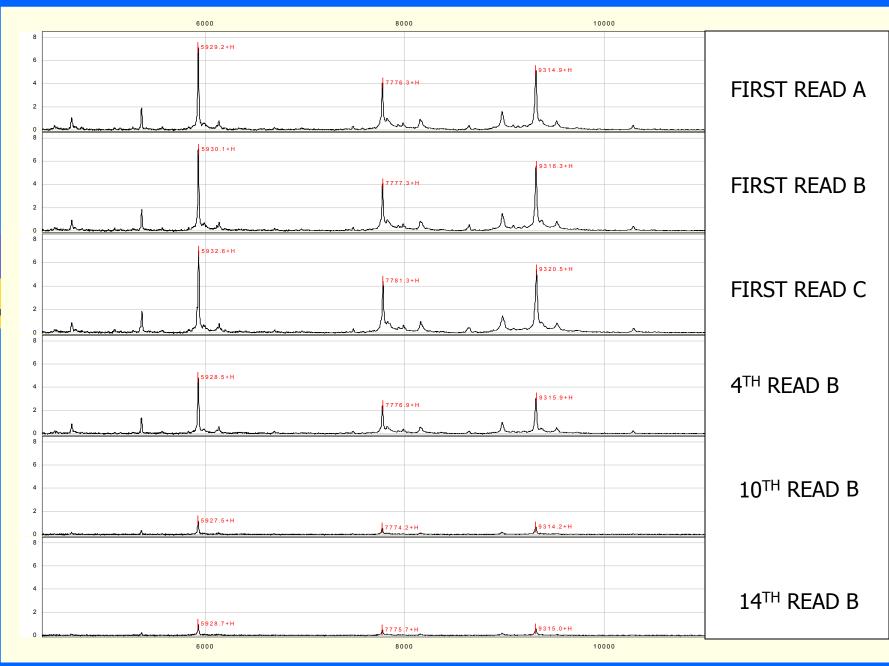
Protein Chip

 High Concentration Proteins May Block Binding of Low Concentration Proteins: 10,000 Ci of 5500 D Protein vs. 10 Ci of 7500 D Protein both with Same Binding Characteristics

Protein Chip

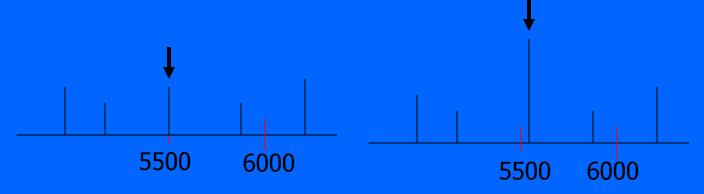
All Proteins/Peptides Bound to Chip May Not Be Released/Ionized.

QC Sample Spectra at Multi-times Reading



Spectrum

- "Directed" and "Non-Directed" Approaches to Begin Spectral Analysis
- Directed= Peak at 5500 Same As Peak at 5507 Based on Resolution +0.2%



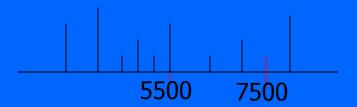
Spectrum

Primary Peaks- Disease Has Unique or Larger Peak than Non-Disease; Thus, the Disease Produces a Molecular Product.

Secondary Peak-Disease Causes a
 Decrease in Molecular Species Normally
 Present via Change in Metabolism or
 Excretion and/or Shutdown in Production

Spectrum

 Components of Spectra at Molecular Weights of Less Than 20,000 May Represent Metabolites of Proteins/Peptides Rather Than Intact Proteins/Peptides



Spectrum

Peaks May Not Provide Independent Information: For Example the Peak at 5500 D May Be A Metabolite of the Peak at 7500





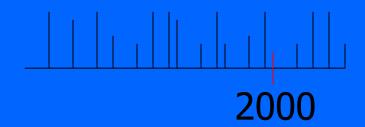
Spectrum

A High Concentration Protein May
 Prevent Identification of Low
 Concentration Protein: 1200 Ci of 5500
 D Protein vs. 100 Ci of 5510 D Protein
 Even with Different Binding
 Characteristics to Same Chip



Spectrum

- All Areas of the Spectrum Are Not The Same
 - Molecular Weights of Less Than 2000
 - No Standards; Noise; Contamination
 - Weights of Greater Than 50,000
 - Proteins of High Concentration



Spectrum

How Variable Is The Peak Location and/or Amplitude When the Same Sample Is Run On the Same Day on the Same Machine? On the Next Day on the Same Machine? On a Different Machine?



Spectrum

- Eastern Virginia Medical School; UAB; U of Texas San Antonio; U of Pittsburgh Medical Center; Johns Hopkins Medical Center; Uniformed Health Services
- All Were Able To Standardize Their
 Machines and To Obtain Comparable
 Data on 14 Cancer and 14 Non Cancer Cases